RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/576,496_

Source: _/FWP,_

Date Processed by STIC: _5/1/06_

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RAW SEQUENCE LISTING   DATE: 05/01/2006
PATENT APPLICATION: US/10/576,496   TIME: 11:00:04

Input Set : A:\Q94468 Sequence Listing.txt
Output Set: N:\CRF4\05012006\J576496.raw

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 3 <110> APPLICANT: Teijin Pharma Limited
 4        Komori, Toshihisa
 5        Kanatani, Naoko
 6        Yoshida, Carolina Andrea
 7        Zanma, Akira
 8        Kobayashi, Shinji
 9        Yamana, Kei
11 <120> TITLE OF INVENTION: BONE AND/OR JOINT-DISEASE-ASSOCIATES GENES
13 <130> FILE REFERENCE: Q94468
15 <140> CURRENT APPLICATION NUMBER: US/10/576,496
15 <141> CURRENT FILING DATE: 2006-04-20
15 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/015879
16 <151> PRIOR FILING DATE: 2004-10-20
18 <150> PRIOR APPLICATION NUMBER: JP 2003-359172
19 <151> PRIOR FILING DATE: 2003-10-20
21 <160> NUMBER OF SEQ ID NOS: 114
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 5220
27 <212> TYPE: DNA
28 <213> ORGANISM: Mouse
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (274)..(1962)
35 <400> SEQUENCE: 1
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38 ccggcagctc cacacagcag aacgccctgg gtccctgaaa ctcgaaaccc gggctcagaa    120
40 ccagcggaaa ccaaagcgaa atccttgaac ttctctgaac aattgcttcc gggcgtttgc    180
42 tgagagccgg gggacctgac cggagcccag gccgcgtatg gcgcgcccct gatgtcacac    240
44 ggacgccagc gaggccagcg ctccggctgc agc atg gac cgc gcg ggg cgc ctg     294
45                                     Met Asp Arg Ala Gly Arg Leu
46                                      1               5
48 ggt gcg ggc ctg cgg gga ctc tgc gtg gct gca ctc gtg ctc gtg tgc     342
49 Gly Ala Gly Leu Arg Gly Leu Cys Val Ala Ala Leu Val Leu Val Cys
50          10              15                  20
52 gcc gga cac ggg ggc cgc cgc gag gat ggg gga cca gct tgc tac gga     390
53 Ala Gly His Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly
54      25              30                  35
56 gga ttc gac ctc tac ttc atc ctg gac aag tca gga agt gtg ctg cac     438
57 Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His
58 40              45                  50                      55
60 cac tgg aat gaa atc tac tac ttc gtg gag cag ttg gct cat aga ttc     486
61 His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Arg Phe
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65 Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly
66                  75                  80                  85
68 aca act tta atg aaa cta act gag gac agg gaa cag atc cga caa ggc       582
69 Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly
 70          90                  95                 100
72 cta gaa gag ctc cag aaa gtt ctg cca gga gga gac act tac atg cac       630
73 Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His
74        105                 110                 115
76 gaa gga ttc gag agg gcc agt gag cag att tac tat gag aac agt caa       678
77 Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Ser Gln
78 120                 125                 130                 135
80 gga tac agg acg gcg agc gtc atc atc gcg ttg acg gat ggg gag ctg       726
81 Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu
82                 140                 145                 150
84 cac gag gac ctc ttc ttc tac tca gag agg gag gct aac cga tcc cga       774
85 His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg
 8          155                 160                 165
88 gac ctt ggt gcg att gtt tac tgc gtt ggc gtg aag gat ttc aat gaa       822
89 Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu
90        170                 175                 180
92 act cag ttg gct cgg att gca gac agt aag gac cac gtg ttt cct gtg       870
93 Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val
94        185                 190                 195
96 aac gac ggc ttc cag gct ctc caa ggc att atc cac tca att tta aag       918
97 Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys
98 200                 205                 210                 215
100 aaa tcc tgc atc gaa att ctg gcg gct gaa cca tcc acc atc tgc gcg      966
101 Lys Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala
102                 220                 225                 230
104 gga gag tcc ttt caa gtg gtc gta aga gga aat ggc ttc cga cat gcc     1014
105 Gly Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala
106                 235                 240                 245
108 cgc aat gtg gac agg gtc ctc tgc agc ttc aaa atc aat gac tca gtc     1062
109 Arg Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val
110         250                 255                 260
112 acg ctc aat gag aag ccc ttt gct gtg gaa gac act tat ttg ctg tgc     1110
113 Thr Leu Asn Glu Lys Pro Phe Ala Val Glu Asp Thr Tyr Leu Leu Cys
114        265                 270                 275
116 cca gca cca atc ttg aaa gaa gtt ggc atg aaa gct gca ctg cag gtc     1158
117 Pro Ala Pro Ile Leu Lys Glu Val Gly Met Lys Ala Ala Leu Gln Val
118 280                 285                 290                 295
120 agc atg aac gac ggc ctg tcc ttc atc tcc agt tct gtc atc atc acc     1206
121 Ser Met Asn Asp Gly Leu Ser Phe Ile Ser Ser Ser Val Ile Ile Thr
122                 300                 305                 310
124 acc aca cac tgt tca gac ggc tcc atc ctg gcg att gct ctg ctg gtc     1254
125 Thr Thr His Cys Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Val
126        315                 320                 325
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128 ctc ttc ctg ctg ctg gcc ctg gcg ctg ctc tgg tgg ttc tgg ccc ctc   1302
129 Leu Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp Trp Phe Trp Pro Leu
130         330             335             340
132 tgc tgc aca gtg atc atc aag gag gtc cct cca ccc cct gtt gag gag   1350
133 Cys Cys Thr Val Ile Ile Lys Glu Val Pro Pro Pro Pro Val Glu Glu
134         345             350             355
136 agt gag gaa gaa gac gat gat ggt ttg cca aag aag aaa tgg ccc aca   1398
137 Ser Glu Glu Glu Asp Asp Asp Gly Leu Pro Lys Lys Lys Trp Pro Thr
138 360             365             370             375
140 gta gat gcc tct tat tat ggt gga cgc ggt gtg gga ggc att aaa aga   1446
141 Val Asp Ala Ser Tyr Tyr Gly Gly Arg Gly Val Gly Gly Ile Lys Arg
142         380             385             390
144 atg gag gtc cgc tgg gga gaa aag ggc tcc aca gaa gaa ggg gcg aag   1494
145 Met Glu Val Arg Trp Gly Glu Lys Gly Ser Thr Glu Glu Gly Ala Lys
146         395             400             405
148 tta gaa aag gca aag aat gca cga gtc aag atg cca gag caa gaa tat   1542
149 Leu Glu Lys Ala Lys Asn Ala Arg Val Lys Met Pro Glu Gln Glu Tyr
150         410             415             420
152 gag ttc cca gaa ccc aga aac ctc aac aac aac atg cgc cgg cct tcc   1590
153 Glu Phe Pro Glu Pro Arg Asn Leu Asn Asn Asn Met Arg Arg Pro Ser
154         425             430             435
156 tcg cct cgg aag tgg tac tcg ccc atc aag gga aaa ctc gat gcc ttg   1638
157 Ser Pro Arg Lys Trp Tyr Ser Pro Ile Lys Gly Lys Leu Asp Ala Leu
158 440             445             450             455
160 tgg gtt ctg ctg aga aaa gga tat gac cga gtg tct gtg atg agg cca   1686
161 Trp Val Leu Leu Arg Lys Gly Tyr Asp Arg Val Ser Val Met Arg Pro
162         460             465             470
164 cag cca gga gac acg gga cgc tgt atc aac ttc acc aga gtg aag aac   1734
165 Gln Pro Gly Asp Thr Gly Arg Cys Ile Asn Phe Thr Arg Val Lys Asn
166         475             480             485
168 agt cag cca gcc aag tat ccc ctg aac aac acc tac cac ccc agc tcc   1782
169 Ser Gln Pro Ala Lys Tyr Pro Leu Asn Asn Thr Tyr His Pro Ser Ser
170         490             495             500
172 cca cct ccc gct cct atc tac aca ccc cca ccc cct gct ccc cac tgc   1830
173 Pro Pro Pro Ala Pro Ile Tyr Thr Pro Pro Pro Pro Ala Pro His Cys
174         505             510             515
176 cct ccc cca gcc ccc agt gcc ccc act cct ccc att cct tcc cca cca   1878
177 Pro Pro Pro Ala Pro Ser Ala Pro Thr Pro Pro Ile Pro Ser Pro Pro
178 520             525             530             535
180 tcc act ctc ccc cct cct cct cag gcc cca ccc cct aac agg gca cct   1926
181 Ser Thr Leu Pro Pro Pro Pro Gln Ala Pro Pro Pro Asn Arg Ala Pro
182         540             545             550
184 ccc ccc tcc cga cct cct cca agg cct tct gtc tag aacccaaagt       1972
185 Pro Pro Ser Arg Pro Pro Pro Arg Pro Ser Val
186         555             560
188 ccgagctctg ggctgcctga gcaactccag caggaggctt ctctgctgaa agaaagatct   2032
190 gcccagccta tgtggtgagt ggcggctgat gtttgcacga tttaaaagca agtcgtgatg   2092
192 ggcagaacaa aatgggcatt ttgaactgcc tgaagacaga caatgagaca ataacagtca   2152
194 cattatagcc tgtgacccct cacctctaga ggaaggttcc cgagatggcc acattgccac   2212
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202 gtgcagtgtc cctagtatgc atcgaatagg tatccaactg ggatctgcag gttgccttat 2452
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234 tattaatcaa tctcagcact agttctcaat ttaatccaat tatattttc cacagtactt 3412
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260 tatggctaga agtttctaga aaccgtcaag gttaatacct ttcagagtag gtgattacag 4192
262 gcaggaagag ctttgatgtg gtttacaaag cccatcagtt ctgtgtcatt ccctgtaagc 4252
264 aacaggagat ggtggttgtg attagcaaac tgcatgtgtt atttgtttga ctccttgtta 4312
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290 tcttctcttt ttctatggta atttagttat ggacgttcag cgtctctgag ttattgttat 5092
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302 <213> ORGANISM: Mouse
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315         35                  40                  45
318 Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val
319     50                  55                  60
322 Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln Leu Arg Met Ser Phe
323 65                  70                  75                  80
326 Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp
327                 85                  90                  95
330 Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro
331             100                 105                 110
334 Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln
335             115                 120                 125
338 Ile Tyr Tyr Glu Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile
339     130                 135                 140
342 Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu
343 145                 150                 155                 160
346 Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val
347             165                 170                 175
350 Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
351             180                 185                 190
354 Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly
355         195                 200                 205
358 Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala
359     210                 215                 220
362 Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg
363 225                 230                 235                 240
366 Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser
367             245                 250                 255
370 Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ala Val
371             260                 265                 270
374 Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
375         275                 280                 285
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379     290                 295                 300
382 Ser Ser Ser Val Ile Ile Thr Thr His Cys Ser Asp Gly Ser Ile
383 305                 310                 315                 320
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VERIFICATION SUMMARY
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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date